

#3

Hi Ms Nh H Nh Ei N M Ms B N H N BB Nh N H N M H N M NEv H/B EiM K

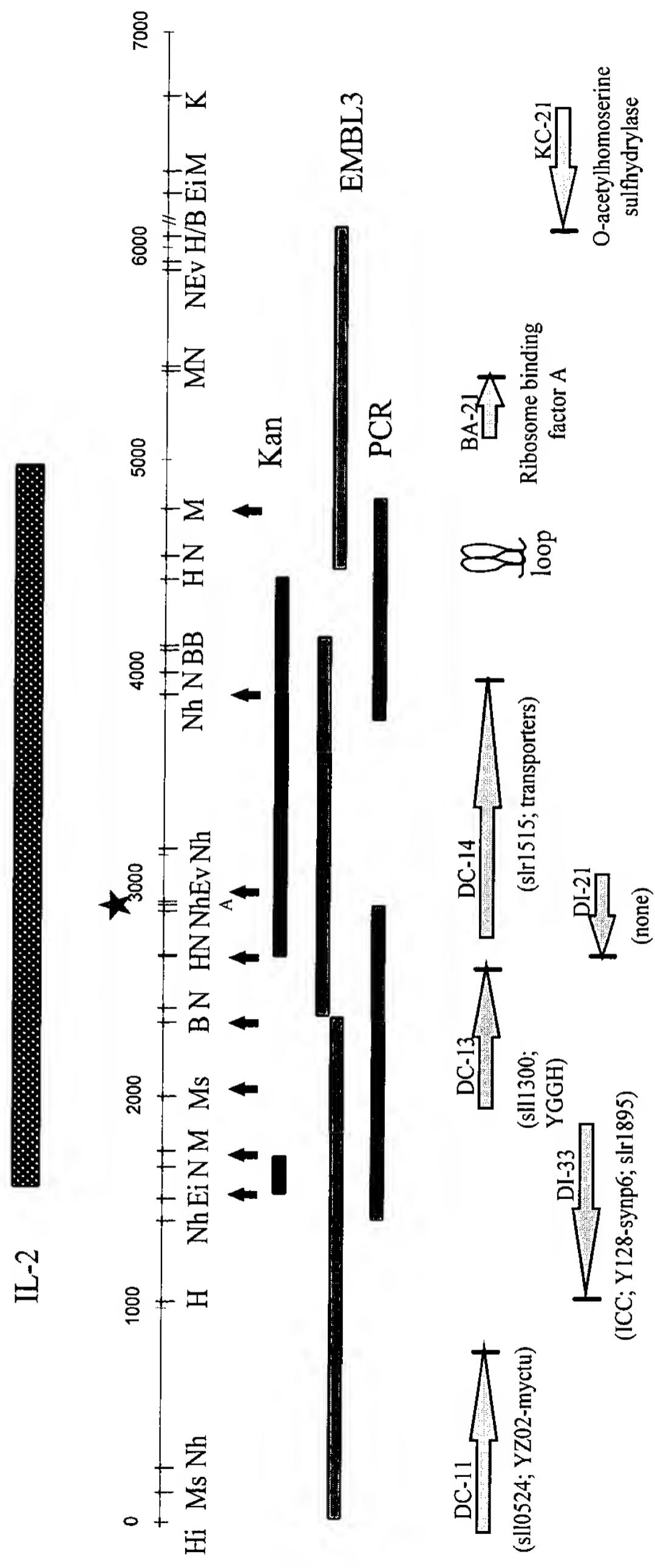


Fig. 1

ICTB :	1	ATGACTGTCTGCCAAACTCTGACTTTGCCATTACCAACCCCCAACAGTGGGCCACACGC	60 (SEQ ID NO:2)
SLR :	13	ATCTCTATCTGGCGATCGCTGATGTTGGGGTTTCCCCCAGGAATGGGGGGCC	72 (SEQ ID NO:4)
ICTB :	61	AGTTTCTGCATGGCCTGTTGGCAGGCCCTGC-GAGGCTTGGGGCCCTCCAGCCAGCTGTT	119
SLR :	73	AGTGTGCTCCATCGTTGGGGCTACGGCT-CAGAG-TGGATAACGGCTACTGCTCCTCTG	131
ICTB :	120	GGTTGGCTGAGGCACTGGCT--GGCTTCTTGCTGCTCTACGGTTCGGCTCCG	177
SLR :	132	GCCCCACTTCGAGGCATTGGGTACGGCT-CTAG-TGGCAATAATTTTTATTGGGCTCCC	189
ICTB :	178	TTTGTGCCCAAGTTCCGCCCTAGGGTAGGGCTAGCCGGATCGCG-GCCTATTGGGCCCT	236
SLR :	190	TTCACCTCCACCAACCATTGGCATTTTAT-GCTGCTCTGGAGCCTTTAGTT	248
ICTB :	237	GCTCTCGCTGACAGATATCGATCTGGCAAGCA---ACCCCCATTCACTGGCTGGTGCT	293
SLR :	249	GCTGACCTTGTGCTGAT--CAACCAG-GGAAGGGTTGACTCCATCCATTGTTAGTT	305
ICTB :	294	GCTCTACTGGGGCTGGATGCCCTAGGAACGGGACTCTCACGGCTGCAGCTTT	353
SLR :	306	TGCCTACTGGTCATTTGGGATCGCCGTGGGATTTCGGTAAAATGGGGGGCC	365
ICTB :	354	AGTTGGCTAGCCAACACTGAC-GCTC-TACCTGTTGGTTTGCCTAGGGCTGGGTT	411
SLR :	366	GTCGGGGTTAGCGAAATTACAGCTAATTGTTCTAC-TGGGGCGAGGTTA	423
ICTB :	412	CTCCGCAATCCCCGTCTGC-GATCGCTGCTGGTCTCGGTGATCACATGGCTTT	470
SLR :	424	TTGCAAAACAAATGGTGAAC-CGGTTAGTAACCGTTACTGGTAGGGCTATT	482

Fig. 2

Fig. 2
(Continued)

ICTB : 943 AACTCCGGATCAATTGTCGGCTGGCGGATGATTCAAGATCGGCCCTGGCTG 1002
 ||| ||||| ||||| ||||| |||||
 SLR : 955 AATTCCGCATCAATTGTTGGCAAAGGGTAAAGCCATGATCCGAGGCCGCCATT 1014

ICTB : 1003 GGCATGGCCCCAATAACCGCCTTAACCTGGTTATCCCTCTATCACACAGGGGCC 1062
 ||| ||||| ||||| ||||| ||||| ||||| |||||
 SLR : 1015 GGCAATTGGCCCTGAGGTACGAAGCCATTAAACCAATTATCCTTACTATAACGGGGTAGTT 1074

ICTB : 1063 TTTACGGCGTTGAGCCCTRACTCCGCTGGAAAGTCCGGTTGAGGGGACTACTG 1122
 ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 SLR : 1075 TTCACCCGCCCTGAGTCAGTGCCTATTCCATTACTAGAAATTGGTGAACGGGTGTAGTT 1134

ICTB : 1123 GGCTTGA-CGGCCTTCGCTTGCGCT-GCTGGTCACGGGGTGACSGCGGGCAGG 1180
 ||| ||| ||| ||| ||| ||| ||| ||| |||
 SLR : 1135 GGTTTACCTGTATGCTC-TGGCTGGCCGGTTAACCTAGGCAAAGGC-GTAGAACTGG 1192

ICTB : 1181 TGAGCCGACTTGGCGGATCGCAATCCCC--AGGCCTTTGGTGTGCTAGCTTGGC 1238
 ||| ||| ||| ||| ||| ||| ||| ||| |||
 SLR : 1193 TTAAACG-CTGTCGC-CAAAACCCTGGGGAGGCATCTGGATTATGGGGCTTGGC 1250

ICTB : 1239 CGGTGGCAGGAATTGCTGGTCACGGCTCTTGTACCCGTCTATGACCCGAAAGC 1298
 ||| ||| ||| ||| ||| ||| ||| |||
 SLR : 1251 GGCGATCATCGGTTGGTCCACGGCATGGTAGATACTGCTGGTACCGTCCCCGGT 1310

ICTB : 1299 CAGTACGGCTCTGGCTCTGTATTGG--AGCGATCGCGAGTTCTGG--CAGC-CCCAA 1353
 ||| ||| ||| ||| ||| ||| |||
 SLR : 1311 GAGCACTTTGGCTGGG-CATTG-TTGCTAGTGGCCATTG-TTGCTAGTCAGTGGGCCAG 1368

ICTB : 1354 CCTTCCAAGCAACTCCCTCCAGAACCGGATTAGACGAA 1395
 ||| ||| ||| ||| |||
 SLR : 1369 GCCCGTTGGAGGCCAGTAAAGAA---GAAAATGAGGACAAA 1407

Fig. 2
(Continued)

SLR : 5 + + W+ + L F + PQ+WG S LHRL G + +W +S L EALG L+A++ +APF
 ISIWRSLMFGGGFSPQEWGRGSVILHRLVGWQGSWITQASVILEPHEALGTALVAIIFIAAPF 64

ICTB : 61 VPFSSALCGLAAIAAYWALLSLTDIDLROATPIHMLVLLYWGVDALATGLSPVRAAALVY 120
 ++ LG+ + A+WALL+ D + TPIH LV YN + A+A G SPV+ AA G

SLR : 65 TSTTMLCGIFMLLCGAFWALLTFADQPGKGLTPHIYLVEAYWCISAIAVGFSPVKMAAASC 124

ICTB : 121 LAKLTLYLLVFAALARVLRNPRLRSLLFSSVVITSLSLFVSVYGLNQWIYGVEELATWVDRN 180
 LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + CVE+LATW D

SLR : 125 LAKLTANLCLFLAARLLQMKQWLNRLLVTVVLLVGLLVSYGLRQQVYDGEVQLATWNDPT 184

ICTB : 181 SVADFTSRVSYLGNPNLLLAAYLVPPTAFAFSAAAIGVWIRGWLPRKLLAATGASSLCLLT 240
 S +RVYS+LGNPNLLLAAYLVP T S +A+ VWR W PKLL + LCL T

SLR : 185 STLAQATRVSFLGNPNLLLAAYLVPMTGSLSLSAIYVWRRWMPKLLIGATMVIVNLCLFFT 244

ICTB : 241 YSRGGWILGFVAMIFVWALLGLYWFQOPRLPA2WRRWLFPWVVLGCLVAVLGLPLEPLRV 300
 SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+

SLR : 245 QSRGGWILAVLALGATFLALCYFWMLPQLPKFWQRWSLPLAIAVAVIILGGGALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSNNFRINWLAFLQMIQDREWLGIGPGNTAFTNLVYPLYQQARFTALSA 360
 R +SIF GREDDSSNNFRINW V MI+ RP +GIGPGN AFN +YP Y + RFTALSA

SLR : 305 RAMSIFAGREDDSSNNFRINWEGVKAMIRARPIIGIGPGNEAFNQIYPPYYMRPRFTALSA 364

ICTB : 361 YSVPLEVAEGGLLGLTAFAWLLVTTAVRQVSRRLRRDRNPKAFWILMASLAGAGMLG 420
 YS+ LE+ VE G+G T WLL VT V V R R+ P+ W+M +LA + G+L

SLR : 365 YSIYLBILVETGVYGETCMWLLAWTLGKGVELVKRCRQTLAPEGIWIMGALAARIIGLLV 424

ICTB : 421 HGLFDTFLYRPEASTLWMLCIGAIASFWQPOPSKQLPPEAEHSDEKM 467
 HG+ DTV YRP STLMWL + +AS W ++ + E+ D+ +

SLR : 425 HGMVDTWVYRPPVSTLWLLVAVSQWASAQARLEASKEENEDKPL 471

Fig. 3

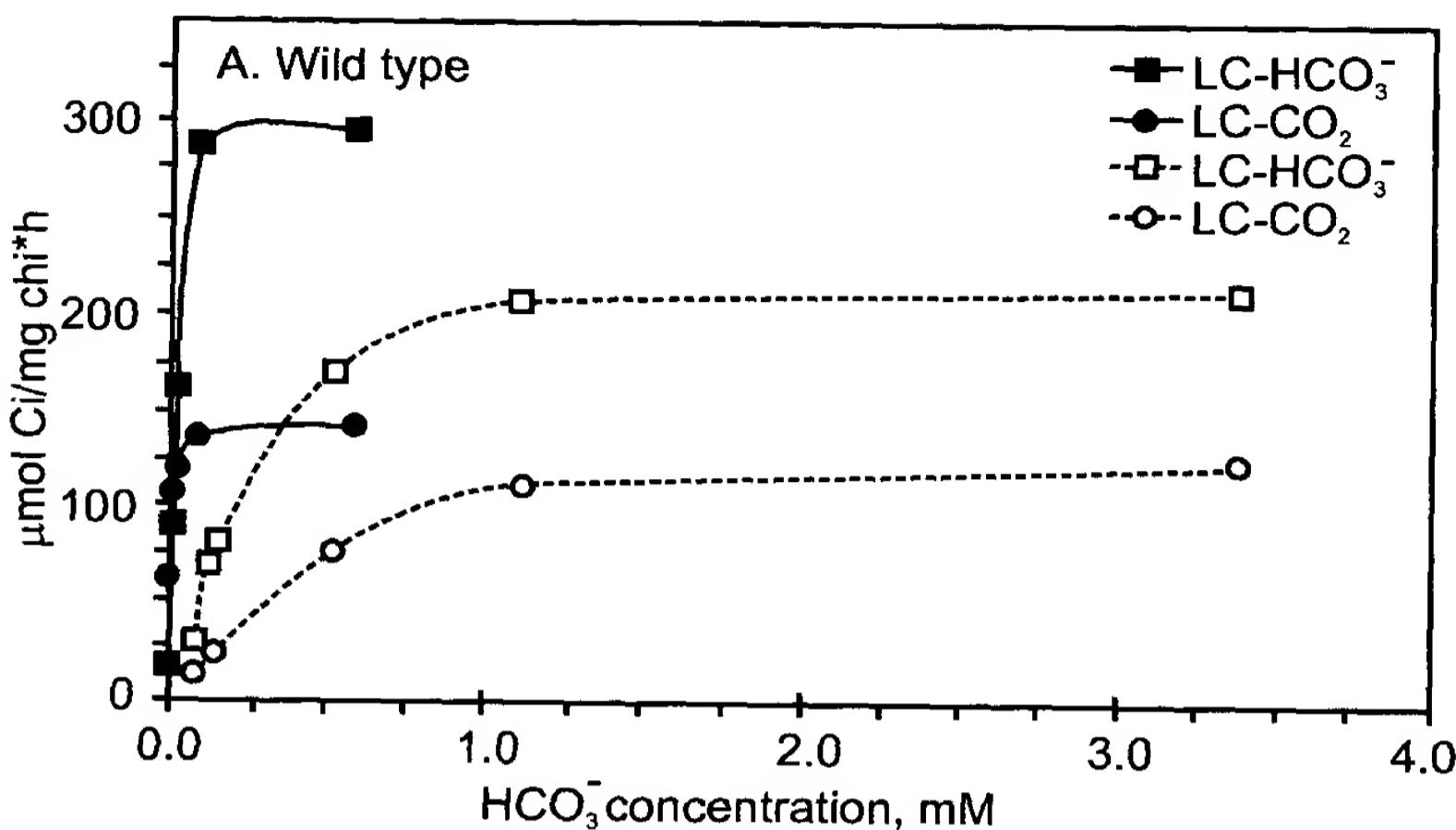


Fig. 4a

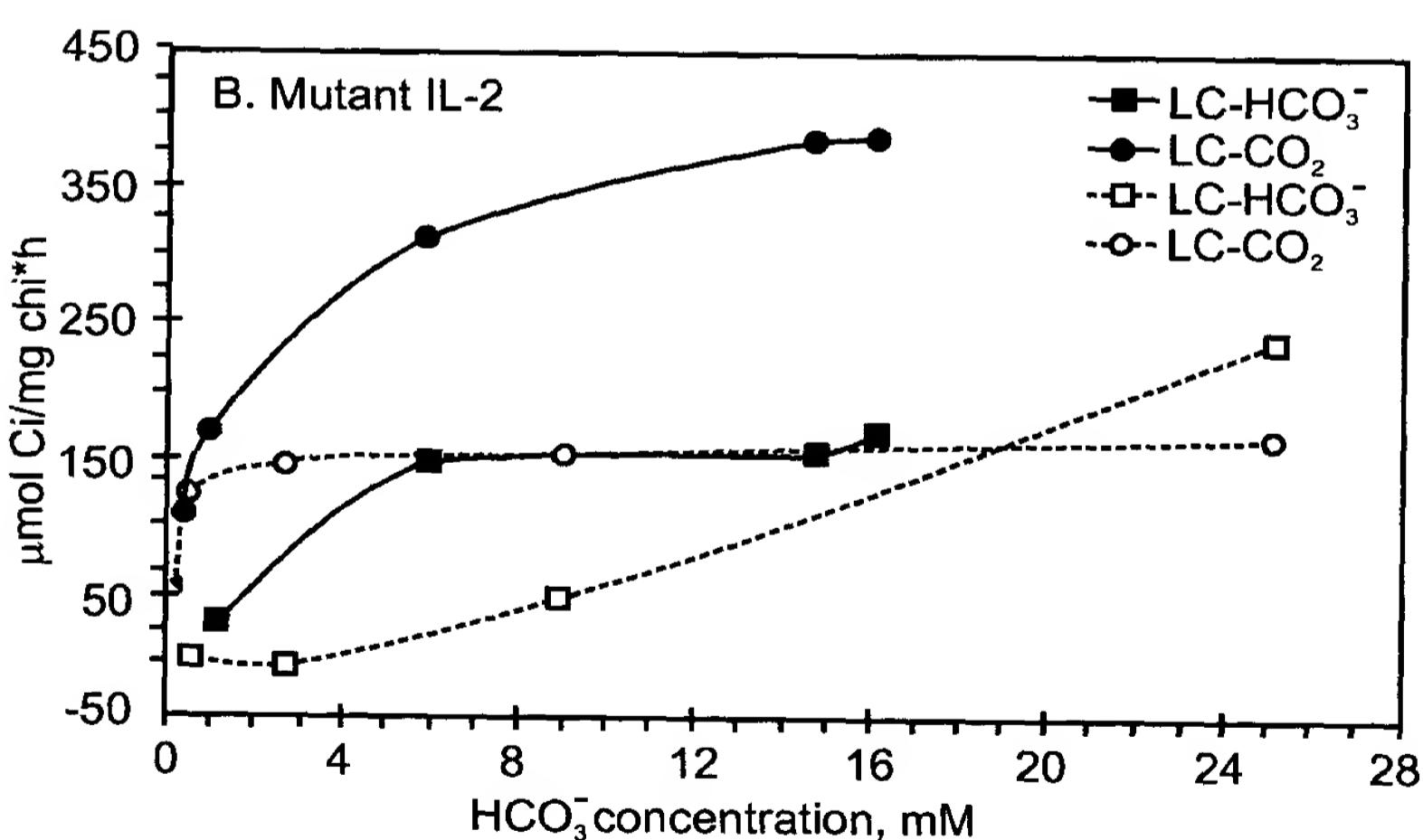


Fig. 4b

Wild type GGGCT-AGCCCGCGA'FCGGCCCTATTGGGCC (SEQ ID NO: 6)
IL-2 ApaI side GGGCT-AG--G-GATCGC-GCCTATTGGGCC (SEQ ID NO: 7)
IL-2 BamHI side GGCTCA-----GATCGC-GCCTATTGGGCC (SEQ ID NO: 8)
IctB G L A A I A A Y W A L (SEQ ID NO: 9)

Fig. 5

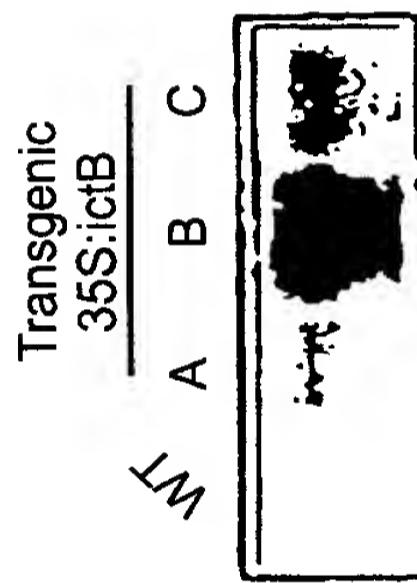


Fig. 6